```
1    AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA   59
                                                          MetPro    2

60   AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC  119
3    ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr   22

120  ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC  180
23   ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu   43

181  ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT  239
44   IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu   62

240  CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG  300
63   HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg   83

301  GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT  359
84   AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro  102

360  GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG  420
103  AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro              118

421  AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC  479
```

FIG. 1A

#4

480 ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC 540
541 AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA 599
600 TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA 660
661 GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT 719
720 GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG 780
781 AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG 839
840 GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT 900
901 CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC 959
960 CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG 1020
1021 GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG 1079
1080 CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT 1140
1141 AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA 1199
1200 TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT 1260
1261 GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC 1319
1320 AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT 1380
1381 AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG 1439
1440 TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG 1500
1501 AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIG. 1B

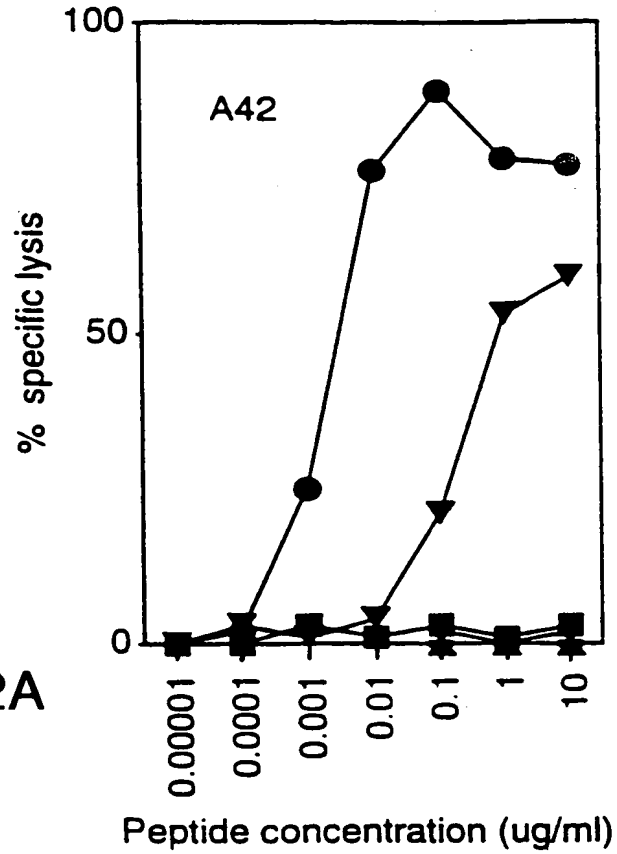

100
50
0
A42
% specific lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2A

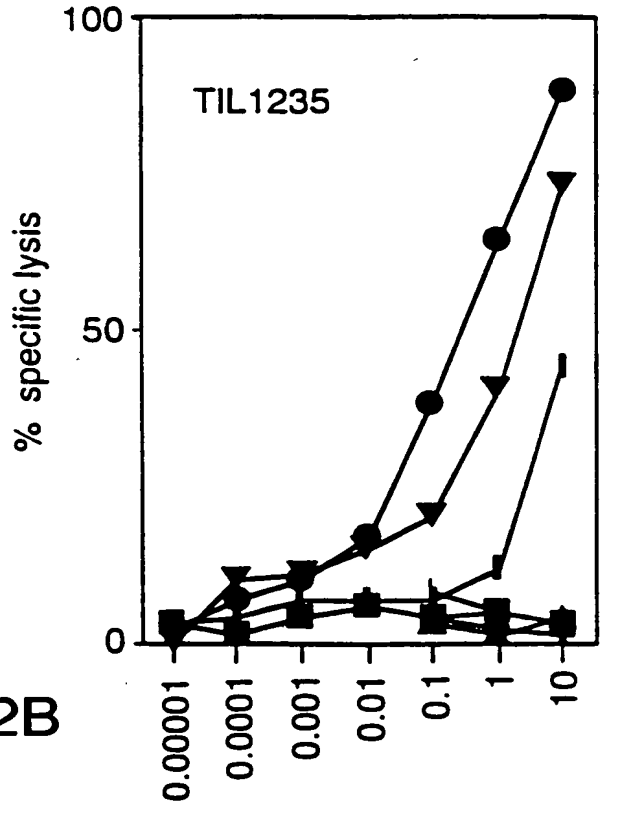

100
50
0
TIL1235
% specific lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2B

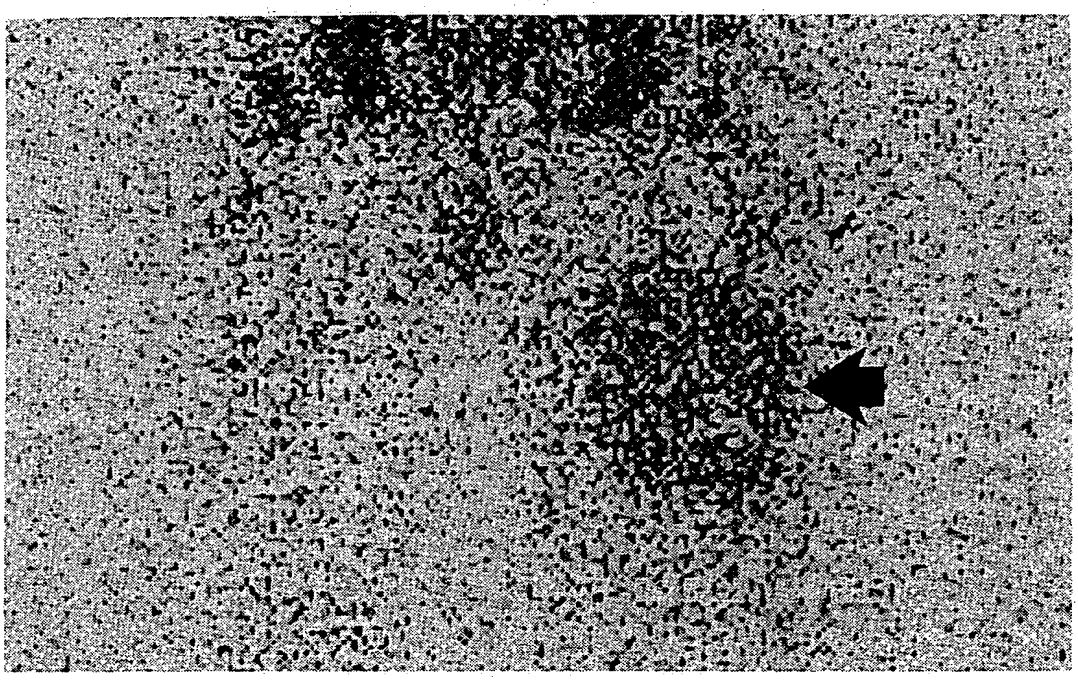


FIG. 3A

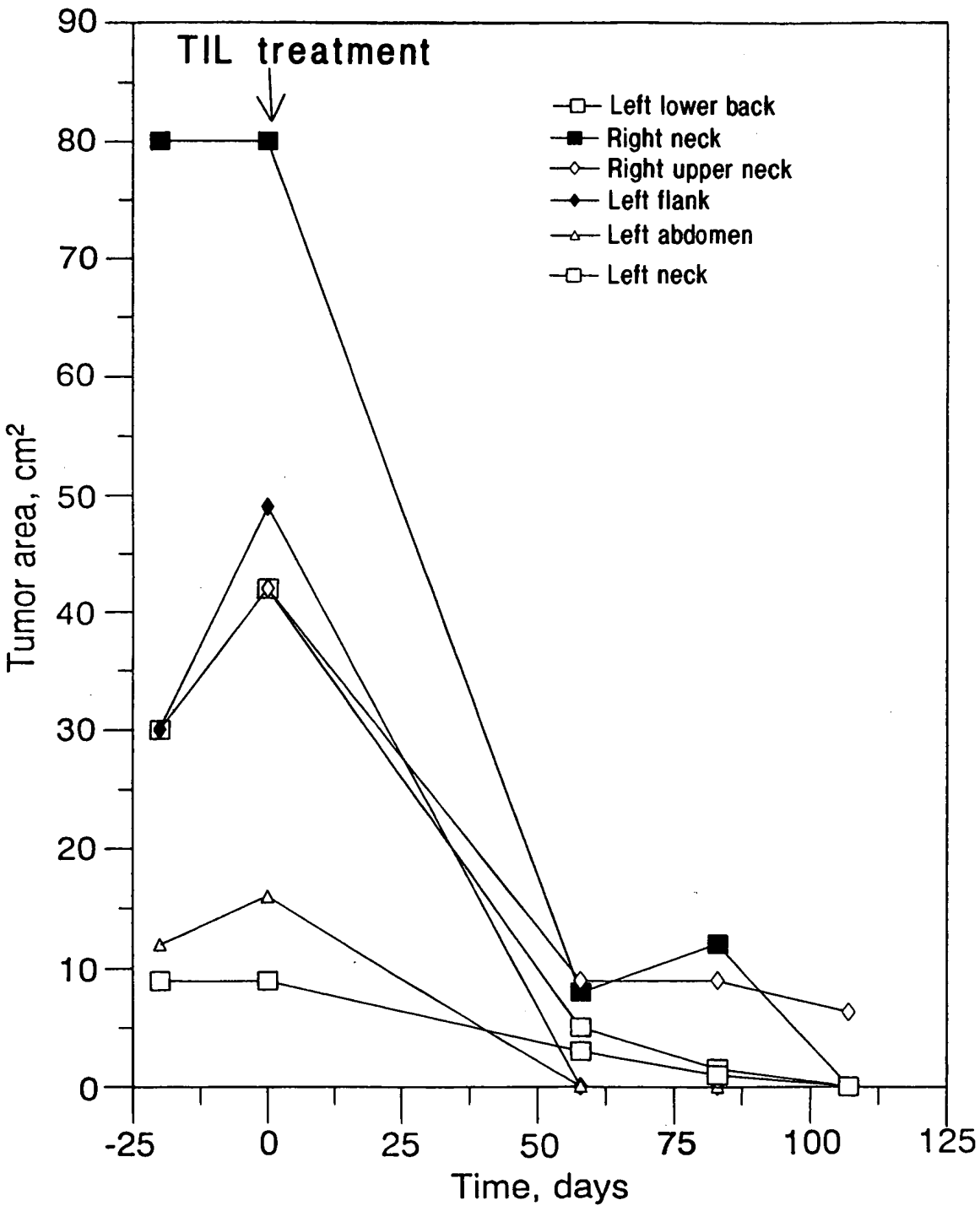
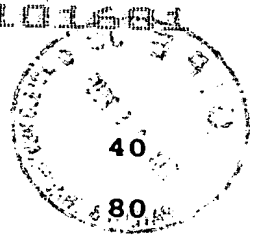
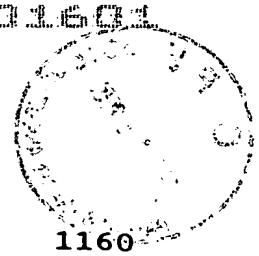

TIL treatment
Left lower back
Right neck
Right upper neck
Left flank
Left abdomen
Left neck
Tumor area, cm2
Time, days
90
80
70
60
50
40
30
20
10
0
-25
0
25
50
75
100
125

FIG. 3B



```
GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT      40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG      80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA     120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC     160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA     200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC     240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA     280
TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA     320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA     360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT     400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT     440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA     480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA     520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA     560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG     600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC     640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT     680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG     720
GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC     760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT     800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA     840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT     880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT     920
GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG     960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA    1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT    1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA    1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC    1120
```

FIG. 4A



TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIG. 4B

```
  1   MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51   EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101   QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151   YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201   AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251   LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301   CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351   VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401   TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451   TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501   AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551   QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601   GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651   ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20        M-----V-----Q-----L----- .....------------
gp100       M-----V-----Q-----L-----.....------------
cDNA25FL    M-----F-----Q-----L-----.....------------
cDNA25TR                  Q-----L----------.....-----PPQWAAGLSTLI
            1     162    236    274    588          649
```

FIG. 5B

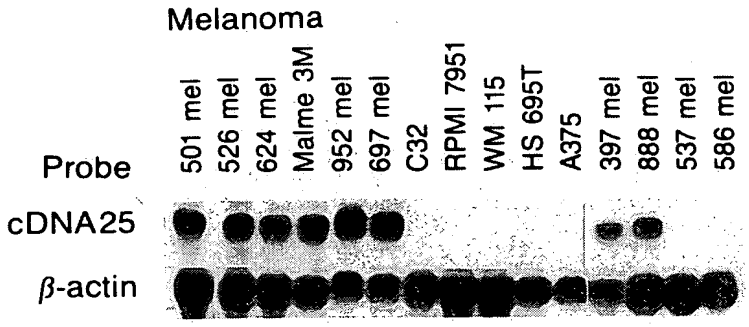


FIG. 6A

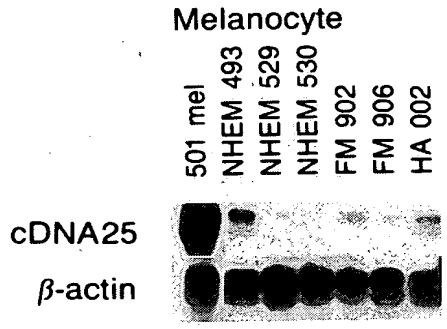


FIG. 6B

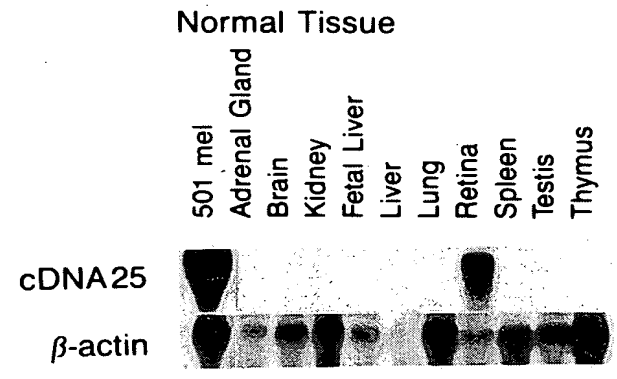


FIG. 6C